

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

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For CRF Submission Help, call (703) 308-4212

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Technical Assistance.....703-287-0200

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<110>  
 <120>  
 <130>  
 <140>  
 <141>  
 <160>

MANDATORY ~~sequence identifier and~~ *response needed for a U.S. filing*  
 delete

09/214881

Since the U.S.  
 filing date was after  
 July 1, 1998, this format  
 Does Not Comply is invalid  
 Corrected Diskette Needed

please ensure all  
 American numbers are  
 aligned under every  
 5 amino acids. Do NOT  
 use TAB code between  
 amino acids

Please  
 follow format  
 shown in

attached sample  
 sequence listing.

Many responses  
 are no longer  
 used under the  
 new sequence rules.

Please consult  
 new sequence rules  
 for valid format.

SEQUENCE LISTING

<210> ~~SEQ ID NO: 1~~  
 <211> ~~LENGTH: 214~~  
 <212> ~~TYPE: amino acid~~ PRT > <213> Human  
 <220> ~~MOLECULAR TYPE: Peptide~~  
 <223> ~~FEATURE: FHM-1~~  
 <223> ~~ORIGINAL SOURCE: Human~~  
 <400> ~~SEQUENCE 1~~  
 Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
                   5                  10                  15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn  
                   20                  25                  30                  35  
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys  
                   40                  45                  50  
 Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg  
                   55                  60                  65                  70  
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp  
                   75                  80                  85                  90  
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr  
                   95                  100                  105  
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys  
                   110                  115                  120                  125  
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro Tyr Glu  
                   130                  135                  140  
 Lys Lys Ala Ala Lys Leu Lys Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
                   145                  150                  155                  160  
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser  
                   165                  170                  175                  180  
 Lys Lys Lys Lys Glu Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu  
                   185                  190                  195  
 Glu Glu Asp Glu Glu Asp Glu Asp Glu Glu Glu Asp Asp Asp Asp Glu  
                   200                  205                  210

<210> ~~SEQ ID NO: 2~~  
 <211> ~~LENGTH: 208~~  
 <212> ~~TYPE: amino acid~~ PRT > <213>  
 <220> ~~MOLECULAR TYPE: Peptide~~  
 <223> ~~FEATURE: FHM-2~~  
 <223> ~~ORIGINAL SOURCE: Human~~  
 <400> ~~SEQUENCE 2~~  
 Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
                   5                  10                  15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn  
                   20                  25                  30                  35  
 Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys  
                   40                  45                  50  
 Glu Lys Ser Lys Phe Glu Asp Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg  
                   55                  60                  65                  70  
 Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp  
                   75                  80                  85                  90  
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His  
                   95                  100                  105  
 Arg Pro Lys Ile Lys Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys  
                   110                  115                  120                  125  
 Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu

Please review the  
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
 <223> fields of each sequence which presents at least one n or Xaa.

130            135            140  
 Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
 145            150            155            160  
 Ala Lys Gly Lys Ser Glu Ala Gly Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser  
 165            170            175            180  
 Lys Lys Lys Asn Glu Pro Glu Asp Glu Glu Glu Glu Glu Glu Asp Glu  
 185            190            195  
 Asp Glu Glu Glu Glu Asp Glu Asp Glu Glu  
 200            205

SEQ ID NO F,R  
 LENGTH F214  
 TYPE Famino acid  
 MOLECULAR TYPE Fpeptide  
 FEATURE FHMG-1  
 ORIGINAL SOURCE FBovine  
 SEQUENCE

*Edti*

*delete*

~~@@@~~ Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
 5            10            15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn  
 20            25            30            35  
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys  
 40            45            50  
 Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg  
 55            60            65            70  
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp  
 75            80            85            90  
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr  
 95            100            105  
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys  
 110            115            120            125  
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro Tyr Glu  
 130            135            140  
 Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
 145            150            155            160  
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser  
 165            170            175            180  
 Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu  
 185            190            195  
 Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Asp Asp Asp Glu  
 200            205            210

SEQ ID NO F,S  
 LENGTH F214  
 TYPE Famino acid  
 MOLECULAR TYPE Fpeptide  
 FEATURE FHMG-1  
 ORIGINAL SOURCE FPorcine  
 SEQUENCE

Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
 5            10            15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn  
 20            25            30            35  
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys  
 40            45            50

Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg  
 55            60            65            70  
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp  
 75            80            85            90  
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr  
 95            100            105  
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys  
 110            115            120            125  
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys His Pro Tyr Glu  
 130            135            140  
 Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
 145            150            155            160  
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser  
 165            170            175            180  
 Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu  
 185            190            195  
 Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Asp Asp Glu  
 200            205            210

SEQ ID NO F,T  
 LENGTH F214  
 TYPE Famino acid  
 MOLECULAR TYPE Fpeptide  
 FEATURE FHMG-1  
 ORIGINAL SOURCE FRat  
 SEQUENCE

Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
 5            10            15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn  
 20            25            30            35  
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys  
 40            45            50  
 Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg  
 55            60            65            70  
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp  
 75            80            85            90  
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr  
 95            100            105  
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys  
 110            115            120            125  
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys His Pro Tyr Glu  
 130            135            140  
 Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
 145            150            155            160  
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser  
 165            170            175            180  
 Lys Lys Lys Lys Glu Glu Glu Asp Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu  
 185            190            195  
 Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Asp Asp Glu  
 200            205            210

SEQ ID NO F,U  
 LENGTH F209  
 TYPE Famino acid  
 MOLECULAR TYPE Fpeptide

## FEATURE FHMG-2

ORIGINAL SOURCE FPorcine

## SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
           5          10          15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn  
   20          25          30          35  
 Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys  
       40          45          50  
 Glu Lys Ser Lys Phe Glu Asp Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg  
   55          60          65          70  
 Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp  
       75          80          85          90  
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His  
       95          100          105  
 Arg Pro Lys Ile Lys Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys  
   110          115          120          125  
 Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu  
       130          135          140  
 Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
   145          150          155          160  
 Ala Lys Gly Lys Gly Glu Ala Gly Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser  
       165          170          175          180  
 Lys Lys Lys Asn Glu Pro Glu Asp Glu Glu Glu Glu Glu Glu Glu Asp  
       185          190          195  
 Glu Asp Glu Glu Glu Glu Asp Glu Asp Glu Glu  
       200          205

SEQ ID NO F,V

LENGTH F186

TYPE F amino acid

FEATURE Fpeptide

FEATURE Fpartial sequence of HMG-2

ORIGINAL SOURCE FBovine

## SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
           5          10          15  
 Val Gln Thr Ser Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn  
   20          25          30          35  
 Phe Ser Glu/Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Ser Lys Phe Glu Asp  
       40          45          50  
 Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg Glu Met Lys Asn Tyr Val Pro  
   55          60          65          70  
 Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp Pro Asn Ala Pro Lys Arg Pro  
       75          80          85          90  
 Pro Ser Ala Phe Phe Leu Phe Ser Ala Glu His Arg Pro Lys Ile Lys Ala Glu  
       95          100          105  
 His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys Lys Leu Gly Glu Met Trp Ser  
   110          115          120          125  
 Gln Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu Gln Lys Ala Ser Lys Leu Lys  
       130          135          140  
 Glu Lys Tyr Glu Lys Xaa Ala Ala Tyr Arg Ala Lys Gly Lys Ser Glu Ala Gly  
   145          150          155          160  
 Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser Lys Lys Lys Asn Glu Pro Glu Asp  
       165          170          175          180

Glu Glu Glu Glu Glu Glu  
185

SEQ ID NO F,W

LENGTH F209

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FEATURE FHMG-2

ORIGINAL SOURCE FRat

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
5 10 15  
Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn  
20 25 30 35  
Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys  
40 45 50  
Glu Lys Ser Lys Phe Glu Asp Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg  
55 60 65 70  
Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp  
75 80 85 90  
Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His  
95 100 105  
Arg Pro Lys Ile Lys Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys  
110 115 120 125  
Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu  
130 135 140  
Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
145 150 155 160  
Ala Lys Gly Lys Ser Glu Val Gly Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser  
165 170 175 180  
Lys Lys Lys Asn Glu Pro Glu Asp Glu Glu Glu Glu Glu Glu Asp Asp  
185 190 195  
Glu Asp Glu Glu Glu Glu Asp Glu Asp Glu Glu  
200 205

SEQ ID NO F,X

LENGTH F206

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FEATURE FHMG-2

ORIGINAL SOURCE FChicken

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Tyr Phe  
5 10 15  
Val Gln Thr Cys Pro Arg Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn  
20 25 30 35  
Phe Ala Glu Phe Ser Arg Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ser Lys  
40 45 50  
Glu Lys Gly Lys Phe Glu Glu Met Ala Lys Gly Asp Lys Ala Arg Tyr Asp Arg  
55 60 65 70  
Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Glu Lys Lys Gly Lys Lys Lys Asp  
75 80 85 90  
Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His  
95 100 105  
Arg Pro Lys Ile Lys Asn Asp His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys

110            115            120            125  
 Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu  
           130            135            140  
 Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg  
 145            150            155            160  
 Ala Lys Ser Lys Ser Asp Ala Gly Lys Lys Gly Pro Gly Arg Pro Ala Gly Ser  
           165            170            175            180  
 Lys Lys Lys Ala Glu Pro Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu  
           185            190            195  
 Glu Glu Glu Glu Glu Asp Glu Glu  
       200            205

SEQ ID NO F,P,O

LENGTH F201

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FEATURE FHMG-2a 

ORIGINAL SOURCE FChicken

SEQUENCE

Ala Lys Gly Asp Pro Lys Lys Pro Lys Gly Lys Met Ser Ala Tyr Ala Phe Phe  
           5            10            15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Asn Pro Glu Val Pro Val Asn  
       20            25            30            35  
 Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ser Lys  
           40            45            50  
 Glu Lys Ala Lys Phe Asp Glu Met Ala Lys Ala Asp Lys Val Arg Tyr Asp Arg  
       55            60            65            70  
 Glu Met Lys Asp Tyr Gly Pro Ala Lys Gly Gly Lys Lys Lys Lys Asp Pro Asn  
           75            80            85            90  
 Ala Pro Lys Arg Pro Pro Ser Gly Phe Phe Leu Phe Cys Ser Glu Phe Arg Pro  
           95            100            105  
 Lys Ile Lys Ser Thr Asn Pro Gly Ile Ser Ile Gly Asp Val Ala Lys Lys Leu  
       110            115            120            125  
 Gly Glu Met Trp Asn Asn Leu Ser Asp Gly Glu Lys Gln Pro Tyr Asn Asn Lys  
           130            135            140  
 Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Val Ala Asp Tyr Lys Ser Lys  
       145            150            155            160  
 Gly Lys Phe Asp Gly Ala Lys Gly Ala Ala Thr Lys Ala Ala Arg Lys Lys Val  
           165            170            175            180  
 Glu Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Asp Glu Asp Asp  
           185            190            195  
 Asp Asp Glu  
       200

SEQ ID NO F,P,P

LENGTH F208

TYPE Famino acid

MOLECULAR TYPE Fpeptide

ORIGINAL SOURCE FMouse

FEATURE FHMG-2

SEQUENCE

Gly Lys Gly Asp Pro Ile Lys Pro Leu Gly Lys Met Ser Ser Tyr Ala Phe Phe  
           5            10            15  
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asn Ser Ser Val Asn  
       20            25            30            35

Phe Ala Glu Ile Ser Lys Lys Cys Ser Lys Arg Trp Lys Thr Met Ser Ala Lys  
           40          45          50  
 Glu Asn Ser Lys Phe Glu Asp Leu Ala Lys Ser Asp Lys Ala Cys Tyr Tyr Arg  
   55          60          65          70  
 Glu Met Lys Asn Tyr Val Ser Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp  
   75          80          85          90  
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Cys Leu Phe Cys Ser Glu Asn  
           95          100          105  
 Arg Pro Lys Ile Lys Ile Glu Tyr Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys  
   110          115          120          125  
 Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Glu Lys Gln Pro Tyr Glu  
   130          135          140  
 Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Phe Ala Ala Tyr Arg 145          150  
 155          160  
 Val Lys Gly Lys Ser Glu Ala Gly Lys Lys Gly Pro Gly Arg Pro Ala Gly Ser          165          170  
 175          180  
 Lys Lys Lys Asn Asp Ser Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu          185          190  
 195  
 Asp Glu Glu Gly Glu Glu Glu Asp Glu Glu  
   200          205

SEQ ID NO F,P,Q

LENGTH F32

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FRAGMENT TYPE FN-terminal fragment of 28KDa

ORIGINAL SOURCE

CELL TYPE Fneutrophil-type cell derived from promyelocytic leukemia

CELL LINE Fneutrophil-type cell line (ATCC CCL-240)

FEATURE

IDENTIFICATION METHOD F,d

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
           5          10          15  
 Val Gln Thr Xaa Arg Glu Glu His Lys Lys Lys His Pro Asp  
   20          25          30

SEQ ID NO F,P,R

LENGTH F32

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FRAGMENT TYPE FN-terminal fragment of 29KDa

ORIGINAL SOURCE

CELL TYPE Fneutrophil-type cell derived from promyelocytic leukemia

CELL LINE Fneutrophil-type cell line (ATCC CCL-240)

FEATURE

IDENTIFICATION METHOD F,d

SEQUENCE

Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe  
           5          10          15  
 Val Gln Thr Xaa Arg Glu Glu His Lys Lys Lys His Pro Asp  
   20          25          30

KA016

-67-